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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/10/006,394

DATE: 01/28/2002  
 TIME: 11:32:53

Input Set : N:\Crf3\RULE60\10006394.raw  
 Output Set: N:\CRF3\01282002\J006394.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Yi Li and Mark D. Adams

7 (ii) TITLE OF INVENTION: Human G-Protein Receptor HIBEF51

9 (iii) NUMBER OF SEQUENCES: 10

11 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: Carella, Byrne, Bain, Gilfillan,  
 Cecchi, Stewart & Olstein

14 (B) STREET: 6 Becker Farm Road

15 (C) CITY: Roseland

16 (D) STATE: NJ

17 (E) COUNTRY: US

18 (F) ZIP: 07068-1739

## 21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: WordPerfect 5.1

## 27 (vi) CURRENT APPLICATION DATA:

C--&gt; 28 (A) APPLICATION NUMBER: US/10/006,394

C--&gt; 29 (B) FILING DATE: 10-Dec-2001

30 (C) CLASSIFICATION:

## 32 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: 09/228,420

34 (B) FILING DATE:

## 36 (viii) ATTORNEY/AGENT INFORMATION:

37 (A) NAME: MULLINS, J.G.

38 (B) REGISTRATION NUMBER: 33073

39 (C) REFERENCE/DOCKET NUMBER: 325800-453 (PF187)

## 41 (ix) TELECOMMUNICATION INFORMATION:

42 (A) TELEPHONE: 201-994-1700

43 (B) TELEFAX: 201-994-1744

## 46 (2) INFORMATION FOR SEQ ID NO: 1:

## 48 (i) SEQUENCE CHARACTERISTICS:

49 (A) LENGTH: 2764 base pairs

50 (B) TYPE: nucleic acid

51 (C) STRANDEDNESS: single

52 (D) TOPOLOGY: linear

## 54 (ii) MOLECULE TYPE: cDNA

## 57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

59 AATTACAGGT AACATTCTGA AATTGAACTA AACAGTAAAT TCTGTTGAAA TGTTTCAAA 60

61 GAGGCAAAAT ATTATATTGG ATCAATGAA GAAAGTAAAT TATCTTGGCT AATTTTATTA 120

63 GTGGTAATTG TAGTGAAAGG TTTCCCTAAA TATTATAAGC AAATTCCTTT TCTCCCCGT 180

ENTERED

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65	CTCAAATGAA	AGGAAATGGG	GGTAAATTAA	TCTGACTGTG	ATTGGTTTG	TTTTATGCTG	240
67	ATCTTGAAG	CTTGATGTTG	CTGCTGCTCC	TCATACAGTA	CAGATCAGTT	GTGTGGGTG	300
69	CTATTGAGGG	TAGCCGTGAA	TAATGGTGCC	AGTAGGGGTG	GAGCGGGAGG	GATGATGCCA	360
71	GCCTGAGCTA	GCCAGGTTCT	TTGATTAGGG	CATTGGATGT	GAAATGTAAA	ATGCTCTCTC	420
73	CTTTTCTTCT	ATCAGCTGTT	CAGAGGAGAC	TCATTACAAC	TCCTGCTGAA	GCTCCTAAC	480
75	TTCTTCCCCCT	CTCTTCTTAC	CTTCCCCCT	ACCCTCACTT	GGCCTGAAGA	CGTTCTCCCC	540
77	AGAGTTTAC	TTGCTCCCCCT	GGTGTATGT	GTATGGTGA	CCTGGCACTA	TGGCCGCGTC	600
79	TGGGACTGGC	CAGACAAC	CTGCTGGCTC	TCCTTATTCC	AGGAAGGATT	TAAAGGGGAA	660
81	TTGCACTGCA	GGCAATGCAC	CAGAGCAGCA	GCATCAGGAG	CTTGGGGAGT	AAGGCTCCTC	720
83	TGGCATTATT	ACACACATGC	AAAGCTGACC	GCAATGACAG	CAGCTGCTTC	TTTGAACGT	780
85	TGGCAGCAGC	CAAGCGGCAG	CATGAAGTGA	CAGATCACTC	CTGAGCTCAA	G ATG AAC	837
86						Met Asn	
88	TCC ACC TTG GAT	GGT AAT CAG	AGC AGC CAC	CCT TTT TGC	CTC TTG GCA		885
89	Ser Thr Leu Asp	Gly Asn Gln	Ser Ser His Pro	Phe Cys Leu	Lau Ala		
90	5	10	15				
92	TTT GGC TAT TTG	GAA ACT GTC	AAT TTT TGC	CTT TTG GAA	GTA TTG ATT		933
93	Phe Gly Tyr Leu	Glu Thr Val Asn	Phe Cys Leu	Lau Glu Val	Lau Ile		
94	20	25	30				
96	ATT GTC TTT CTA	ACT GTA TTG	ATT ATT TCT	GGC AAC ATC	ATT GTG ATT		981
97	Ile Val Phe Leu	Thr Val Leu Ile	Ile Ser Gly	Asn Ile Ile Val	Ile		
98	35	40	45	50			
100	TTT GTA TTT CAC	TGT GCA CCT	TTG AAC CAT	CAC ACT ACA	AGT TAT		1029
101	Phe Val Phe His	Cys Ala Pro	Leu Leu Asn	His His Thr	Thr Ser Tyr		
102	55	60	65				
104	TTT ATC CAG ACT	ATG GCA TAT	GCT GAC CTT	TTT GTT GGG	GTG AGC TGC		1077
105	Phe Ile Gln Thr	Met Ala Tyr	Ala Asp Leu	Phe Val Gly	Val Ser Cys		
106	70	75	80				
108	GTG GTC CCT TCT	TTA TCA CTC	CTC CAT CAC CCC	CTT CCA G	TA GAG GAG		1125
109	Val Val Pro Ser	Leu Ser Leu	His His Pro	Leu Pro	Val Glu		
110	85	90	95				
112	TCC TTG ACT TGC	CAG ATA TTT	GGT TTT GTA	GTA TCA GTT	CTG AAG AGC		1173
113	Ser Leu Thr Cys	Gln Ile Phe	Gly Phe Val	Val Ser Val	Lau Lys Ser		
114	100	105	110				
116	GTC TCC ATG GCT	TCT CTG GCC	TGT ATC AGC	ATT GAT AGA	TAC ATT GCC		1221
117	Val Ser Met Ala	Ser Leu Ala	Cys Ile Ser	Ile Asp Arg	Tyr Ile Ala		
118	115	120	125	130			
120	ATT ACT AAA CCT	TTA ACC TAT	AAT ACT CTG	GTT ACA CCC	TGG AGA CTA		1269
121	Ile Thr Lys Pro	Leu Thr Tyr	Asn Thr	Leu Val Thr	Pro Trp Arg		
122	135	140	145				
124	CGC CTG TGT	ATT TTC CTG	ATT TGG CTA	TAC TCG ACC	CTG GTC TTC		1317
125	Arg Leu Cys Ile	Phe Leu Ile	Trp Leu	Tyr Ser Thr	Leu Val Phe		
126	150	155	160				
128	CCT TCC TTT	TTC CAC TGG	GGC AAA CCT	GGA TAT CAT	GGA GAT GTG		1365
129	Pro Ser Phe	Phe His Trp	Gly Lys Pro	Gly Tyr His	Gly Asp Val Phe		
130	165	170	175				
132	CAG TGG TGT	GCG GAG TCC	TGG CAC ACC	GAC TCC TAC	TTC ACC CTG		1413
133	Gln Trp Cys	Ala Glu Ser	Trp His	Thr Asp Ser	Tyr Phe Thr		
134	180	185	190				
136	ATC GTG ATG ATG	TTA TAT	GCC CCA GCA	GCC CTT ATT	GTC TGC	TTC ACC	1461

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137	Ile	Val	Met	Met	Leu	Tyr	Ala	Pro	Ala	Ala	Leu	Ile	Val	Cys	Phe	Thr		
138	195				200						205					210		
140	TAT	TTC	AAC	ATC	TTC	CGC	ATC	TGC	CAA	CAG	CAC	ACA	AAG	GAT	ATC	AGC	1509	
141	Tyr	Phe	Asn	Ile	Phe	Arg	Ile	Cys	Gln	Gln	His	Thr	Lys	Asp	Ile	Ser		
142					215				220						225			
144	GAA	AGG	CAA	GCC	CGC	TTC	AGC	AGC	CAG	AGT	GGG	GAG	ACT	GGG	GAA	GTG	1557	
145	Glu	Arg	Gln	Ala	Arg	Phe	Ser	Ser	Gln	Ser	Gly	Glu	Thr	Gly	Glu	Val		
146					230				235						240			
148	CAG	GCC	TGT	CCT	GAT	AAG	CGC	TAT	GCC	ATG	GTC	CTG	TTT	CGA	ATC	ACT	1605	
149	Gln	Ala	Cys	Pro	Asp	Lys	Arg	Tyr	Ala	Met	Val	Leu	Phe	Arg	Ile	Thr		
150					245				250						255			
152	AGT	GTA	TTT	TAC	ATC	CTC	TGG	TTG	CCA	TAT	ATC	ATC	TAC	TTC	TTG	TTG	1653	
153	Ser	Val	Phe	Tyr	Ile	Leu	Trp	Leu	Pro	Tyr	Ile	Ile	Tyr	Phe	Leu	Leu		
154					260				265						270			
156	GAA	AGC	TCC	ACT	GGC	CAC	AGC	AAC	CGC	TTC	GCA	TCC	TTC	TTG	ACC	ACC	1701	
157	Glu	Ser	Ser	Thr	Gly	His	Ser	Asn	Arg	Phe	Ala	Ser	Phe	Leu	Thr	Thr		
158					275				280						285		290	
160	TGG	CTT	GCT	ATT	AGT	AAC	AGT	TTC	TGC	AAC	TGT	GTA	ATT	TAT	AGT	CTC	1749	
161	Trp	Leu	Ala	Ile	Ser	Asn	Ser	Phe	Cys	Asn	Cys	Val	Ile	Tyr	Ser	Leu		
162					295				300						305			
164	TCC	AAC	AGT	GTA	TTC	CAA	AGA	GGA	CTA	AAG	CGC	CTC	TCA	GGG	GCT	ATG	1797	
165	Ser	Asn	Ser	Val	Phe	Gln	Arg	Gly	Leu	Lys	Arg	Leu	Ser	Gly	Ala	Met		
166					310				315						320			
168	TGT	ACT	TCT	TGT	GCA	AGT	CAG	ACT	ACA	GCC	AAC	GAC	CCT	TAC	ACA	GTT	1845	
169	Cys	Thr	Ser	Cys	Ala	Ser	Gln	Thr	Thr	Ala	Asn	Asp	Pro	Tyr	Thr	Val		
170					325				330						335			
172	AGA	AGC	AAA	GGC	CCT	CTT	AAT	GGA	TGT	CAT	ATC	TGAAGTGGCT	CAGTTACGGG			1898		
173	Arg	Ser	Lys	Gly	Pro	Leu	Asn	Gly	Cys	His	Ile							
174					340				345									
176	GTT	CCC	GTG	TGT	GTG	TGT	GTG	TGT	GTG	TGT	GTG	TGT	GTG	TGT	GTG	TGT	1958	
178	TAAT	TCATA	GGAA	ATCT	GG	GAC	AGA	ATAC	TTTG	ACT	CTA	AA	CA	ATAG	CA	TACAA	ATTAT	2018
180	TCG	TAT	GGAT	AC	CTT	CTA	AG	TTT	GTAG	AAA	TG	TTT	CC	AA	G	TGT	TGT	2078
182	ACT	CAAG	ATC	ATG	AAG	ACAA	AT	TG	C	TCT	CT	CT	CA	AT	TT	GA	ATG	2138
184	CTAC	AGT	TCT	CAG	ATT	TTA	AAA	TTA	AG	CC	AT	AT	CT	TT	TC	GC	CAT	2198
186	GACT	GAAC	CT	GAG	TGT	GAAA	AG	CG	TCA	TTT	AAA	AG	TC	AT	CT	CA	CT	2258
188	TCT	GGG	C	TCT	TC	AG	CT	AG	TT	GG	GG	GG	CT	TT	CT	GT	CA	2318
190	AAA	AA	TATA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	2378
192	TG	CAAG	TT	TC	AA	AC	AT	GT	AA	AG	CA	AT	GT	TT	TT	TT	AG	2438
194	AAT	TCT	CA	AG	GT	GA	AT	GT	GA	AC	AA	AC	AT	TT	TA	AG	TG	2498
196	ACC	AT	GAAG	CA	AA	AA	GT	CA	AA	TT	AT	AA	TT	GA	AA	CT	GG	2558
198	GCC	AT	GCT	TC	AC	AG	AG	AT	GT	GT	GT	GT	GT	GT	AG	T	TT	2618
200	CCC	AT	GCG	CT	TG	TG	TT	AT	TT	TA	AA	AT	CT	GA	TT	TT	AC	2678
202	AGC	AA	AA	AT	GT	G	CT	TA	AG	CT	AA	AA	TT	G	AT	CG	AT	2738
204	CG	TG	AC	CT	C	G	AG	GG	GG	GG	GG	GG	GG	GG	GG	GG	GG	2764
208	(2)	INFORMATION	FOR	SEQ	ID	NO:	2:											
210		(i)	SEQUENCE	CHARACTERISTICS:														
211			(A)	LENGTH:	349	amino	acids											
212			(B)	TYPE:	amino	acid												
213			(D)	TOPOLOGY:	Linear													

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215 (ii) MOLECULE TYPE: protein  
 217 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 219 Met Asn Ser Thr Leu Asp Gly Asn Gln Ser Ser His Pro Phe Cys Leu  
 220 5 10 15  
 221 Leu Ala Phe Gly Tyr Leu Glu Thr Val Asn Phe Cys Leu Leu Glu Val  
 222 20 25 30  
 223 Leu Ile Ile Val Phe Leu Thr Val Leu Ile Ile Ser Gly Asn Ile Ile  
 224 35 40 45  
 225 Val Ile Phe Val Phe His Cys Ala Pro Leu Leu Asn His His Thr Thr  
 226 50 55 60  
 227 Ser Tyr Phe Ile Gln Thr Met Ala Tyr Ala Asp Leu Phe Val Gly Val  
 228 65 70 75 80  
 229 Ser Cys Val Val Pro Ser Leu Ser Leu Leu His His Pro Leu Pro Val  
 230 85 90 95  
 231 Glu Glu Ser Leu Thr Cys Gln Ile Phe Gly Phe Val Val Ser Val Leu  
 232 100 105 110  
 233 Lys Ser Val Ser Met Ala Ser Leu Ala Cys Ile Ser Ile Asp Arg Tyr  
 234 115 120 125  
 235 Ile Ala Ile Thr Lys Pro Leu Thr Tyr Asn Thr Leu Val Thr Pro Trp  
 236 130 135 140  
 237 Arg Leu Arg Leu Cys Ile Phe Leu Ile Trp Leu Tyr Ser Thr Leu Val  
 238 145 150 155 160  
 239 Phe Leu Pro Ser Phe Phe His Trp Gly Lys Pro Gly Tyr His Gly Asp  
 240 165 170 175  
 241 Val Phe Gln Trp Cys Ala Glu Ser Trp His Thr Asp Ser Tyr Phe Thr  
 242 180 185 190  
 243 Leu Phe Ile Val Met Met Leu Tyr Ala Pro Ala Ala Leu Ile Val Cys  
 244 195 200 205  
 245 Phe Thr Phe Asn Ile Phe Arg Ile Cys Gln Gln His Thr Lys Asp  
 246 210 215 220  
 247 Ile Ser Glu Arg Gln Ala Arg Phe Ser Ser Gln Ser Gly Glu Thr Gly  
 248 225 230 235 240  
 249 Glu Val Gln Ala Cys Pro Asp Lys Arg Tyr Ala Met Val Leu Phe Arg  
 250 245 250 255  
 251 Ile Thr Ser Val Phe Tyr Ile Leu Trp Leu Pro Tyr Ile Ile Tyr Phe  
 252 260 265 270  
 253 Leu Leu Glu Ser Ser Thr Gly His Ser Asn Arg Phe Ala Ser Phe Leu  
 254 275 280 285  
 255 Thr Thr Trp Leu Ala Ile Ser Asn Ser Phe Cys Asn Cys Val Ile Tyr  
 256 290 295 300  
 257 Ser Leu Ser Asn Ser Val Phe Gln Arg Gly Leu Lys Arg Leu Ser Gly  
 258 305 310 315 320  
 259 Ala Met Cys Thr Ser Cys Ala Ser Gln Thr Thr Ala Asn Asp Pro Tyr  
 260 325 330 335  
 261 Thr Val Arg Ser Lys Gly Pro Leu Asn Gly Cys His Ile  
 262 340 345  
 266 (2) INFORMATION FOR SEQ ID NO: 3:  
 268 (i) SEQUENCE CHARACTERISTICS:  
 269 (A) LENGTH: 358 amino acids

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270 (B) TYPE: amino acid  
 271 (C) STRANDEDNESS: Not Relevant  
 W--> 272 (D) TOPOLOGY: Not Relevant  
 274 (ii) MOLECULE TYPE: protein  
 276 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
 W--> 278 Met Asn Ser Thr Leu Xaa Asp Gly Asn Gln Ser Ser His Pro Phe Cys  
 279 5 10 15  
 280 Leu Leu Ala Phe Gly Tyr Leu Glu Thr Val Asn Phe Cys Leu Leu Glu  
 281 20 25 30  
 W--> 282 Val Leu Ile Ile Val Xaa Xaa Xaa Phe Leu Thr Val Leu Ile Ile  
 283 35 40 45  
 284 Ser Gly Asn Ile Ile Val Ile Phe Val Phe His Cys Ala Pro Leu Leu  
 285 50 55 60  
 286 Asn His His Thr Thr Ser Tyr Phe Ile Gln Thr Met Ala Tyr Ala Asp  
 287 65 70 75 80  
 288 Leu Phe Val Gly Val Ser Cys Val Val Pro Ser Leu Ser Leu Leu His  
 289 85 90 95  
 W--> 290 His Pro Leu Pro Xaa Xaa Val Glu Glu Ser Leu Thr Cys Gln Ile Phe  
 291 100 105 110  
 292 Gly Phe Val Val Ser Val Leu Lys Ser Val Ser Met Ala Ser Leu Ala  
 293 115 120 125  
 294 Cys Ile Ser Ile Asp Arg Tyr Ile Ala Ile Thr Lys Pro Leu Thr Tyr  
 295 130 135 140  
 296 Asn Thr Leu Val Thr Pro Trp Arg Leu Arg Leu Cys Ile Phe Leu Ile  
 297 145 150 155 160  
 298 Trp Leu Tyr Ser Thr Leu Val Phe Leu Pro Ser Phe Phe His Trp Gly  
 299 165 170 175  
 300 Lys Pro Gly Tyr His Gly Asp Val Phe Gln Trp Cys Ala Glu Ser Trp  
 301 180 185 190  
 W--> 302 Xaa Xaa Xaa His Thr Asp Ser Tyr Phe Thr Leu Phe Ile Val Met Met  
 303 195 200 205  
 304 Leu Tyr Ala Pro Ala Ala Leu Ile Val Cys Phe Thr Tyr Phe Asn Ile  
 305 210 215 220  
 W--> 306 Phe Arg Ile Cys Gln Gln His Thr Lys Asp Ile Ser Glu Arg Xaa Xaa  
 307 225 230 235 240  
 W--> 308 Xaa Gln Ala Arg Phe Ser  
 309 245 250 255  
 W--> 310 Ser Gln Ser Gly Xaa Xaa Xaa Xaa Glu Thr Gly Glu Val Gln Ala Cys  
 311 260 265 270  
 312 Pro Asp Lys Arg Tyr Ala Met Val Leu Phe Arg Ile Thr Ser Val Phe  
 313 275 280 285  
 314 Tyr Ile Leu Trp Leu Pro Tyr Ile Ile Tyr Phe Leu Leu Glu Ser Ser  
 315 290 295 300  
 316 Thr Gly His Ser Asn Arg Phe Ala Ser Phe Leu Thr Thr Trp Leu Ala  
 317 305 310 315 320  
 318 Ile Ser Asn Ser Phe Cys Asn Cys Val Ile Tyr Ser Leu Ser Asn Ser  
 319 325 330 335  
 320 Val Phe Gln Arg Gly Leu Lys Arg Leu Ser Gly Ala Met Cys Thr Ser  
 321 340 345 350

VERIFICATION SUMMARY  
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Input Set : N:\Crf3\RULE60\10006394.raw  
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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:272 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=3  
L:278 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:290 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:306 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:308 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:310 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:333 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=4  
L:347 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:349 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:361 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:382 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4